Listing of Claims:

This Listing of Claims replaces all the prior listings of claims.

1.-8. (Cancelled)

9. (Original) A method of determining the concentration or the copy number of nucleic acid molecules with rare mutations comprising the steps of:

a) amplifying a nucleic acid sample and a known amount of a control competitive nucleic acid standard sample in the same reaction, wherein the control nucleic acid sample has been designed to have the same sequence as the rare mutation containing amplicon with the exception of one nucleic acid difference immediately adjacent to the mutation site, with primers flanking the mutation site;

b) removing the excess dNTPs;

c) performing a primer extension reaction using a detection primer(s), which is designed so that the 3' end of the primer anneals immediately adjacent to the rare mutation site and in the presence of at least one deoxynucleotide (dNTP) and two dideoxynucleotides (ddNTPs), wherein the dNTP corresponds to the first nucleoside after the 3' end of the detection primer in the nucleic acid with the rare mutation, the first ddNTP corresponds to the nucleoside artificially created to the control which differs from the nucleoside present in the rare mutant allele, and the second ddNTP corresponds to the nucleoside present in the rare mutant allele immediately after the mutation site;

d) detecting the production of primer extension products and/or consumption of ddNTP; and

e) determining the ratio of the amplified rare mutant, wherein the rare mutant includes any change from the wildtype including polymorphisms and the standard competitor and calculating the concentration or copy number of the rare mutant nucleic acid variant in the original sample base on the known amount of the competitor initially added to the amplification reaction in the step a).

10. (Original) The method of claim 9, wherein a mixture of dNTP(s)/ddNTP(s) are used, wherein none of the dNTPs or ddNTPs can also be used for the extension of the wildtype DNA, and the extension product from the rare mutant and the control DNA can be distinguished.

11. (Original) The method of claim 9, wherein the consumption of ddNTPs is quantified.

12. (Canceled)